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TECH CENTER 1605/2900



SEQUENCE LISTING

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<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY  
MODIFIED PLANTS

<130> 20263/255164

<140> 09/117,921

<141> 1999-03-04

<150> 08/597,313

<151> 1996-02-06

<150> PCT/US97/02187

<151> 1997-02-06

<160> 15

<170> PatentIn Ver. 2.1

<210> 1

<211> 543

<212> DNA

<213> Lesquerella fendleri

<220>

<221> primer\_bind

<222> (83)

<223> nucleotide sequence of pLesq2

<400> 1

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ccacctaga aagctgcagt canatggtat gtcaaatacc tcaacaaccc tcttggacgc 120  
attctggtgt taacagttca gtttatcttc ggggtggcctt tgtatctagc ctttaagtga 180  
tcaggtagac cttatgatgg ttctgcttca cattctcttc ctcatgcacc tatctttaag 240  
gaccgtgaac gtctccagat atacatctca gatgctggtt ttctagctgt ctgttatggt 300  
ctttaccgtt acgctgcttc acaaggattg actgctatga tctgctgcta cggagtaccg 360  
cttttgatag tgaacttttt ccttgctctg gtcactttct tgcagcacac tcatccttca 420  
ttacctcact atgattcaac cgagtgggaa tggattagag gagctttggt tacggtagac 480  
agagactatg gaatcttgaa caaggtgttt cacaacataa cagacacca cgtagcacac 540  
cac 543

<210> 2

<211> 544

<212> DNA

<213> Lesquerella fendleri

<400> 2

tataggcacc ggaggcacca ttccaacaca ggatccctcg aaagagatga agtattttgtc 60  
ccaaagcaga aatccgcaat caagtgttac ggcgaatacc tcaacaaccc tcttggctgc 120  
atcatgatgt taactgtcca gttcgtcttc ggatggcctt tgtacttagc cttcaacgtt 180

tctggcagac cctacaatgg ttctgcttcc cattttctcc ccaatgctcc tatctacaac 240  
gaccgtgaac gctccagat ttacatctct gatgctggtt ttctagccgt ctggttatggt 300  
ctttaccgtt acgctgttgc acaaggacta gcctcaatga tctgtctaaa cggagttccg 360  
cttctgatag ttaacttttt cctcgtcttg atcacttact tacaacacac tcacctgcg 420  
ttgcctcact atgattcatc agagtgggat tggcttagag gagcttttagc tactgtagac 480  
agagactatg gaatcttgaa caagggtgtc cataacatca cagacacca cgtcgcacac 540  
cact 544

<210> 3  
<211> 1855  
<212> DNA  
<213> *Lesquerella fendleri*

<220>  
<221> gene  
<222> (1)..(1855)  
<223> genomic clone encoding pLesq-HYD

<400> 3  
atgaagcttt ataagaagtt agttttctct ggtgacagag aaattntgtc aattggtagt 60  
gacagttgaa gcaacaggaa caacaaggat ggttgggtgnt gatgctgatg tggatgatgtg 120  
ttattcatca aatactaaat actacattac ttgttgtctg ctacttctcc tatttcctcc 180  
gccacccatt ttggaccac ganccttcca tttaaaccct ctctcgtgct attcaccaga 240  
agagaagcca agagagagag agagagaatg ttctgaggat cattgtcttc ttcacgtta 300  
ttaacgtaag ttttttttga ccactcatat ctaaaatcta gtacatgcaa tagattaatg 360  
actgttcctt cttttgatat ttccagcttc ttgaattcaa gatgggtgct ggtggaagaa 420  
taatggttac cccctcttcc aagaaatcag aaactgaagc cctaaaacgt ggaccatgtg 480  
agaaaccacc attcactgtt aaagatctga agaaagcaat cccacagcat tgtttcaagc 540  
gctctatccc tcgttcttcc tccctacctc tcacagatat cactttagtt tcttgcttct 600  
actacgttgc cacaaattac ttctctcttc ttccctcagcc tctctctact tacctagctt 660  
ggcctctcta ttgggtatgt caaggtctgt tcttaaccgg tatctgggtc attggccatg 720  
aatgtgggtca ccatgcattc agtgactatc aatgggtaga tgacactgtt ggttttatct 780  
tccattcctt ccttctcgtc ccttacttct cctggaaata cagtcacgt cgtcaccatt 840  
ccaacaatgg atctctcgag aaagatgaag tctttgtccc accgaagaaa gctgcagtca 900  
aatgggtatgt taaatacctc aacaaccctc ttggacgcat tctgggtgta acagttcagt 960  
ttatcctcgg gtggcctttg tatctagcct ttaatgtatc aggtagacct tatgatggtt 1020  
tcgcttcaca tttcttccct catgcacctc tctttaaaga ccgagaacgc ctccagatat 1080  
acatctcaga tgctgggtatt ctactgtctt gttatgggtt ttaccgttac gctgcttcac 1140  
aaggattgac tgctatgatc tgcgtctatg gagtaccgct tttgatagtg aactttttcc 1200  
ttgtcttggt aactttcttg cagcacactc atccttcgtt acctcattat gattcaaccg 1260  
agtgggaatg gattagagga gctttgggtt cggtagacag agactatgga atattgaaca 1320  
aggtgttcca taacataaca gacacacatg tggctcatca tctctttgca actataccgc 1380  
attataacgc aatggaagct acagaggcga taaagccaat acttgggtgat tactaccact 1440  
tcgatggaac accgtgggat gtggccatgt atagggaagc aaaggagtggt ctctatgtag 1500  
aaccggatac ggaacgtggg aagaaagggtg tctactatta caacaataag ttatgaggct 1560  
gatagggcga gagaagtgc attatcaatc ttcatttcca tgttttaggt gtcttggtta 1620  
agaagctatg ctttgtttca ataactcag agtccatnta gttgtgttct ggtgcatttt 1680  
gcctagttat gtggtgtcgg aagttagtgt tcaaactgct tccgtctgtg ctgccagtg 1740  
aagaacaagt ttacgtgttt aaaatactcg gaacgaattg accacaanat atccaaaacc 1800  
ggctatccga attccatata cgaaaaccgg atatccaaat ttccagagta cttag 1855

<210> 4  
<211> 384  
<212> PRT  
<213> *Lesquerella fendleri*

<400> 4

Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser  
1 5 10 15

Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr  
20 25 30

Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser  
35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser  
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
65 70 75 80

Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys  
85 90 95

Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala  
100 105 110

Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His  
115 120 125

Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg  
130 135 140

His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro  
145 150 155 160

Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro  
165 170 175

Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro  
180 185 190

Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala  
195 200 205

Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu  
210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
225 230 235 240

Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr  
245 250 255

Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe  
260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp  
275 280 285

Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile

a!  
cont

290		295		300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His				
305		310		315 320
Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala				
	325		330	335
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp				
	340		345	350
Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro				
	355		360	365
Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu				
	370		375	380

<210> 5  
 <211> 387  
 <212> PRT  
 <213> Ricinus communis

<400> 5

Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser				
1	5		10	15
Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys				
	20		25	30
Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys				
	35		40	45
Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val				
	50		55	60
Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr				
	65		70	75
Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe				
	85		90	95
Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly				
	100		105	110
His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu				
	115		120	125
Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser				
	130		135	140
His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val				
	145		150	155
				160

a!  
cont

Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser  
 165 170 175  
 Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu  
 180 185 190  
 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp  
 195 200 205  
 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg  
 210 215 220  
 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr  
 225 230 235 240  
 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met  
 245 250 255  
 Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met  
 260 265 270  
 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser  
 275 280 285  
 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp  
 290 295 300  
 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val  
 305 310 315 320  
 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala  
 325 330 335  
 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly  
 340 345 350  
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe  
 355 360 365  
 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg  
 370 375 380  
 Asn Lys Tyr  
 385

@!  
 Cont

<210> 6  
 <211> 383  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 6  
 Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser  
 1 5 10 15

Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser  
 20 25 30

Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80  
 Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
 85 90 95  
 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
 100 105 110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
 115 120 125  
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140  
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150 155 160  
 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
 165 170 175  
 Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys  
 195 200 205  
 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr  
 225 230 235 240  
 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 305 310 315 320  
 Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335

a!  
 Cont

Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr  
340 345 350

Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp  
355 360 365

Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
370 375 380

<210> 7

<211> 384

<212> PRT

<213> Brassica napus

<220>

<221> PEPTIDE

<222> (1)..(384)

<223> encodes for hydroxylase enzyme for Brassica napus

<400> 7

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser  
1 5 10 15

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr  
20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
35 40 45

Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser  
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro  
65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe  
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg  
145 150 155 160

Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly  
165 170 175

Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr  
180 185 190

a!  
cont.

Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys  
 195 200 205  
 His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu  
 225 230 235 240  
 Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu  
 305 310 315 320  
 Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val  
 340 345 350  
 Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp  
 355 360 365  
 Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu Xaa  
 370 375 380

<210> 8  
 <211> 309  
 <212> PRT  
 <213> Glycine max

<400> 8  
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 1 5 10 15

Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu Leu Pro Gln Pro  
 20 25 30

Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu  
 35 40 45

Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val

a!  
 cont.



50	55	60
Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr		
65	70	75 80
Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser		
	85	90 95
Leu Asp Arg Asp Glu Arg Val Lys Val Ala Trp Phe Ser Lys Tyr Leu		
	100	105 110
Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile		
	115	120 125
Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp		
	130	135 140
Ser Phe Ala Ser His Tyr His Pro Tyr Arg Val Arg Leu Leu Ile Tyr		
	145	150 155 160
Val Ser Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val		
	165	170 175
Ala Thr Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro		
	180	185 190
Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Arg Val		
	195	200 205
His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr		
	210	215 220
Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr		
	225	230 235 240
Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His		
	245	250 255
Leu Arg Val Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp Thr		
	260	265 270
Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val		
	275	280 285
Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg Asn		
	290	295 300
Lys Tyr Leu Arg Val		
305		

<210> 9  
 <211> 302  
 <212> PRT  
 <213> Glycine max  
  
 <400> 9

Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe Cys Leu Tyr Tyr  
 1 5 10 15  
 Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro Leu Ser Phe Arg  
 20 25 30  
 Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile Leu Thr Gly Val  
 35 40 45  
 Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly  
 50 55 60  
 Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr  
 65 70 75 80  
 Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu  
 85 90 95  
 Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg  
 100 105 110  
 Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu  
 115 120 125  
 Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr  
 130 135 140  
 Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu  
 145 150 155 160  
 Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala  
 165 170 175  
 Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe  
 180 185 190  
 Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp  
 195 200 205  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 210 215 220  
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 225 230 235 240  
 Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Val Glu Tyr  
 245 250 255  
 Tyr Arg Phe Asp Glu Thr Pro Phe Val Lys Ala Met Trp Arg Glu Ala  
 260 265 270  
 Arg Glu Cys Ile Tyr Val Glu Pro Asp Gln Ser Thr Glu Ser Lys Gly  
 275 280 285  
 Val Phe Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala Thr Val  
 290 295 300

a!  
 cont.

<210> 10  
<211> 372  
<212> PRT  
<213> Zea mays

<220>  
<221> PEPTIDE  
<222> (372)  
<223> Desaturase

<400> 10

Met Gly Ala Gly Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu  
1 5 10 15

Gln Leu Ala Arg Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val  
20 25 30

Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro  
35 40 45

His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His  
50 55 60

Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile  
65 70 75 80

Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp  
85 90 95

Ile Ala Gln Gly Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val  
100 105 110

Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys  
115 120 125

Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp  
130 135 140

Glu Val Phe Val Pro Lys Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro  
145 150 155 160

Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln  
165 170 175

Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg  
180 185 190

Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr  
195 200 205

Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val  
210 215 220

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp  
225 230 235 240

a!  
cont.

Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp  
 245 250 255  
 Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His  
 260 265 270  
 Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met  
 275 280 285  
 Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp  
 290 295 300  
 Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala  
 305 310 315 320  
 Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His  
 325 330 335  
 Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu  
 340 345 350  
 Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn  
 355 360 365  
 Lys Lys Phe Xaa  
 370

<210> 11  
 <211> 224  
 <212> PRT  
 <213> Ricinus communis

<400> 11  
 Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln  
 1 5 10 15  
 Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys Leu Leu Val  
 20 25 30  
 Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr  
 35 40 45  
 Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser  
 50 55 60  
 Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met  
 65 70 75 80  
 Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe  
 85 90 95  
 Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro  
 100 105 110  
 Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser  
 115 120 125

a!  
 cont

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile  
 130 135 140  
 Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu  
 145 150 155 160  
 Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His  
 165 170 175  
 Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly  
 180 185 190  
 Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe  
 195 200 205  
 His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro  
 210 215 220

<210> 12  
 <211> 20  
 <212> DNA  
 <213> Ricinus communis

<400> 12  
 gctcttttgt gcgctcatto 20

<210> 13  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: homologous  
 regions of Ricinus communis deduced by hydroxylase  
 sequence and Arabidopsis thaliana deduced desaturase  
 sequence for use as oligonucleotide primer

<400> 13  
 cggtaccaga aaacgccttg 20

<210> 14  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)..(20)  
 <223> n is any nucleotide in mixed oligonucleotide  
 primer

a!  
 cont

<220>

<223> Description of Artificial Sequence: homologous  
regions of Ricinus communis deduced by hydroxylase  
sequence and Arabidopsis thaliana deduced  
desaturase sequence for u

<400> 14

taywsncaym gnmgnca yca

20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: homologous  
regions of Ricinus communis deduced by hydroxylase  
sequence and Arabidopsis thaliana deduced  
desaturase sequence for u

<220>

<221> primer\_bind

<222> (1)..(21)

<223> n is any nucleotide in mixed oligonucleotide  
primer

<400> 15

rtgrtgngcn acrtgngtrt c

21

a!  
cont

